

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

(ii) TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

(iii) NUMBER OF SEQUENCES: 45

(iv) CORRESPONDENCE ADDRESS:
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(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/231,565
(B) FILING DATE: 22-APR-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 2026-4124

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1559
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAGACAGA GGACTCTCAT TAAGGAAGGT GTCCTGTGCC 40
CTGACCCTAC AAGATGCCAA GAGAAGATGC TCACCTTCATC 80
TATGGTTACC CCAAGAACGG GCACGGCCAC TCTTACACCA 120
CGGCTGAAGA GGCGCTGGG ATCGGCATCC TGACAGTGAT 160
CCTGGGAGTC TTACTGCTCA TCGGCTGTTG GTATTGTAGA 200
AGACGAAATG GATACAGAGC CTTGATGGAT AAAAGTCTTC 240
ATGTTGGCAC TCAATGTGCC TTAACAAGAA GATGCCACA 280
AGAAGGGTTT GATCATCGGG ACAGCAAAGT GTCTCTCAA 320
GAGAAAAACT GTGAACCTGT GGTTCCCAAT GCTCCACCTG 360
CTTATGAGAA ACTCTCTGCA GAACAGTCAC CACCACCTTA 400
TTCACCTTAA GAGCCAGCGA GACACCTGAG ACATGCTGAA 440
ATTATTTCTC TCACACTTTT GCTTGAATTT AATACAGACA 480
TCTAATGTT TCCTTTGGAA TGGTGTAGGA AAAATGCAAG 520
CCATCTCTAA TAATAAGTCA GTGTTAAAAT TTTAGTAGGT 560
CCGCTAGCAG TACTAATCAT GTGAGGAAAT GATGAGAAAT 600
ATTAAATTGG GAAAACCTCCA TCAATAAAATG TTGCAATGCA 640
TGATACTATC TGTGCCAGAG GTAATGTTAG TAAATCCATG 680
GTGTTATTTT CTGAGAGACA GAATTCAAGT GGGTATTCTG 720
GGGCCATCCA ATTTCTCTT ACTTGAAATT TGGCTAATAA 760
CAAACAGTC AGGTTTCGA ACCTTGACCG ACATGAACTG 800
TACACAGAAT TGTTCCAGTA CTATGGAGTG CTCACAAAGG 840
ATACTTTTAC AGGTTAACAGAC AAAGGGTTGA CTGGCCTATT 880
TATCTGATCA AGAACATGTC AGCAATGTCT CTTTGTGCTC 920
TAAAATTCTA TTATACTACA ATAATATATT GTAAAGATCC 960
TATAGCTCTT TTTTTTGAG ATGGAGTTTC GCTTTGTTG 1000
CCCAGGCTGG AGTGCAATGG CGCGATCTG GCTCACCATA 1040
ACCTCCGCCT CCCAGGTTCA AGCAATTCTC CTGCCTTAGC 1080

CTCCTGAGTA GCTGGGATTA CAGGCGTGCG CCACTATGCC	1120
TGACTAATTT TGTAGTTTA GTAGAGACGG GGTTTCTCCA	1160
TGTTGGTCAG GCTGGTCTCA AACTCCTGAC CTCAGGTGAT	1200
CTGCCCGCCT CAGCCTCCCA AAGTGCTGGA ATTACAGGCG	1240
TGAGCCACCA CGCCTGGCTG GATCCTATAT CTTAGGTAAG	1280
ACATATAACG CAGTCTAATT ACATTTCACT TCAAGGCTCA	1320
ATGCTATTCT AACTAATGAC AAGTATTTC TACTAAACCA	1360
GAAATTGGTA GAAGGATTTA AATAAGTAAA AGCTACTATG	1400
TACTGCCTTA GTGCTGATGC CTGTGTACTG CCTTAAATGT	1440
ACCTATGGCA ATTTAGCTCT CTTGGGTTCC CAAATCCCTC	1480
TCACAAGAAT GTGCAGAAGA AATCATAAAG GATCAGAGAT	1520
TCTGAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1559

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys		
1	5	10
Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala		
15	20	25
Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu		
30	35	40
Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala		
45	50	55
Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu		
60	65	70

Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser
75 80

Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro
85 90 95

Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110

Pro Pro Pro Tyr Ser Pro
115

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Ile Gly Ile Leu Thr Val Ile Leu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ile Leu Thr Val Ile Leu Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ile Leu Thr Val Ile Leu Gly Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Val Ile Leu Gly Val Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Ile Leu Gly Val Leu Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Ile Leu Gly Val Leu Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Leu Met Asp Lys Ser Leu His Val
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

~~AB~~
Ser Leu His Val Gly Thr Gln Cys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Val Val Pro Asn Ala Pro Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Ala Pro Pro Ala Tyr Glu Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid

(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Gly Ile Gly Ile Leu Thr Val Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Ile Leu Thr Val Ile Leu Gly Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Leu Thr Val Ile Leu Gly Val Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Val Ile Ileu Gly Val Leu Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Val Ile Leu Gly Val Leu Leu Leu Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Ala Leu Met Asp Lys Ser Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Leu His Val Gly Thr Gln Cys Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2172
(B) TYPE: nucleotide
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAA 280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA 320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360
CCATCATCAA TGGGAGCCAG GTGTGGGAG GACAGCCAGT 400

GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480
GCTTTGTTA TGTCTGGAAG ACCTGGGCC AATACTGGCA 520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560
GGCAGGGCAA TGCTGGCAC ACACACCAG GAAGTGACTG 600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680
TTCTCCGTGA GCGTGTCCC GTTGCGGGCC TTGGATGGAG 720
GGAACAAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760
CCTCCAGCTC CATGACCCCCA GTGGCTATCT GGCTGAAGCT 800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920
GCCATTCCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040
ACTACACCTG GTCAGGGGCC AACTGCAGAG CCCTCTGGAA 1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120
TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG 1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA 1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC 1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA 1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG 1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC 1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG 1400
GGCCCCCTGC TGGATGGTAC AGCCACCTA AGGCTGGTGA 1440
AGAGACAAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG 1480

TTCCCTTTCC GTCACCCCTGG ACATTGTCCA GGGTATTGAA 1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG 1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC 1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG 1640
CCCCCTGCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC 1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG 1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATAAC 1760
AACAGCCTGG CAGTGGTCAAG CACCCAGCTT ATCATGCCTG 1800
GTCAAGAACGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880
ATATATAAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920
CCCAGTTGCC ACATAGGCAGG AGTCACTGGC TGCCTCTACC 1960
CCGCATCTTC TGCTCTGTC CCATTGGTGA GAACAGCCCC 2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC 2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAAT 2120
ACTCAGAGCC TGAAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160
AAAAAAAAAA AA 2172

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 661
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu
1 5 10

A
B

Ala	Val	Ile	Gly	Ala	Leu	Leu	Ala	Val	Gly	Ala	Thr
				15				20			
Lys	Val	Pro	Arg	Asn	Gln	Asp	Trp	Leu	Gly	Val	Ser
					30				35		
Arg	Gln	Leu	Arg	Thr	Lys	Ala	Trp	Asn	Arg	Gln	Leu
				40				45			
Tyr	Pro	Glu	Trp	Thr	Glu	Ala	Gln	Arg	Leu	Asp	Cys
				50			55			60	
Trp	Arg	Gly	Gly	Gln	Val	Ser	Leu	Lys	Val	Ser	Asn
					65			70			
Asp	Gly	Pro	Thr	Leu	Ile	Gly	Ala	Asn	Ala	Ser	Phe
				75			80				
Ser	Ile	Ala	Leu	Asn	Phe	Pro	Gly	Ser	Gln	Lys	Val
				85			90			95	
Leu	Pro	Asp	Gly	Gln	Val	Ile	Trp	Val	Asn	Asn	Thr
					100			105			
Ile	Ile	Asn	Gly	Ser	Gln	Val	Trp	Gly	Gly	Gln	Pro
				110		115				120	
Val	Tyr	Pro	Gln	Glu	Thr	Asp	Asp	Ala	Cys	Ile	Phe
					125			130			
Pro	Asp	Gly	Gly	Pro	Cys	Pro	Ser	Gly	Ser	Trp	Ser
				135			140				
Gln	Lys	Arg	Ser	Phe	Val	Tyr	Val	Trp	Lys	Thr	Trp
					145		150			155	
Gly	Gln	Tyr	Trp	Gln	Phe	Leu	Gly	Gly	Pro	Val	Ser
					160		165				
Gly	Leu	Ser	Ile	Gly	Thr	Gly	Arg	Ala	Met	Leu	Gly
				170		175				180	
Thr	His	Thr	Met	Glu	Val	Thr	Val	Tyr	His	Arg	Arg
					185			190			
Gly	Ser	Arg	Ser	Tyr	Val	Pro	Leu	Ala	His	Ser	Ser
				195			200				
Ser	Ala	Phe	Thr	Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser
					205		210			215	
Val	Ser	Val	Ser	Gln	Leu	Arg	Ala	Leu	Asp	Gly	Gly
					220			225			
Asn	Lys	His	Phe	Leu	Arg	Asn	Gln	Pro	Leu	Thr	Phe
					230		235			240	
Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	Leu	Ala
					245			250			
Glu	Ala	Asp	Leu	Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp
				255			260				
Ser	Ser	Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Val	Val
					260		265			270	
Thr	His	Thr	Tyr	Leu	Glu	Pro	Gly	Pro	Val	Thr	Ala
					275			280			
Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser
					285		290			295	
Cys	Gly	Ser	Ser	Pro	Val	Pro	Gly	Thr	Thr	Asp	Gly
					300			305			
His	Arg	Pro	Thr	Ala	Glu	Ala	Pro	Asn	Thr	Thr	Ala
				310			315				
Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Val	Gly	Thr	Thr
					320		325			330	

A
B

Pro	Gly	Gln	Ala	Pro	Thr	Ala	Glu	Pro	Ser	Gly	Thr
			335					340			
Thr	Ser	Val	Gln	Val	Pro	Thr	Thr	Glu	Val	Ile	Ser
	345				350		350			355	
Thr	Ala	Pro	Val	Gln	Met	Pro	Thr	Ala	Glu	Ser	Thr
				360					365		
Gly	Met	Thr	Pro	Glu	Lys	Val	Pro	Val	Ser	Glu	Val
		370				375					
Met	Gly	Thr	Thr	Leu	Ala	Glu	Met	Ser	Thr	Pro	Glu
380					385				390		
Ala	Thr	Gly	Met	Thr	Pro	Ala	Glu	Val	Ser	Ile	Val
		395					400				
Val	Leu	Ser	Gly	Thr	Thr	Ala	Ala	Gln	Val	Thr	Thr
	405				410					415	
Thr	Glu	Trp	Val	Glu	Thr	Thr	Ala	Arg	Glu	Leu	Pro
				420				425			
Ile	Pro	Glu	Pro	Glu	Gly	Pro	Asp	Ala	Ser	Ser	Ile
	430				435						
Met	Ser	Thr	Glu	Ser	Ile	Thr	Gly	Ser	Leu	Gly	Pro
440					445				450		
Leu	Leu	Asp	Gly	Thr	Ala	Thr	Leu	Arg	Leu	Val	Lys
		455				460					
Arg	Gln	Val	Pro	Leu	Asp	Cys	Val	Leu	Tyr	Arg	Tyr
	465					470			475		
Gly	Ser	Phe	Ser	Val	Thr	Leu	Asp	Ile	Val	Gln	Gly
				480				490			
Ile	Glu	Ser	Ala	Glu	Ile	Leu	Gln	Ala	Val	Pro	Ser
		495				500					
Gly	Glu	Gly	Asp	Ala	Phe	Glu	Leu	Thr	Val	Ser	Cys
505					510			515			
Gln	Gly	Gly	Leu	Pro	Lys	Glu	Ala	Cys	Met	Glu	Ile
			520				525				
Ser	Ser	Pro	Gly	Cys	Gln	Pro	Pro	Ala	Gln	Arg	Leu
	530					535				540	
Cys	Gln	Pro	Val	Leu	Pro	Ser	Pro	Ala	Cys	Gln	Leu
				545			550				
Val	Leu	His	Gln	Ile	Leu	Lys	Gly	Gly	Ser	Gly	Thr
				555		560					
Tyr	Cys	Leu	Asn	Val	Ser	Leu	Ala	Asp	Thr	Asn	Ser
565					570				575		
Leu	Ala	Val	Val	Ser	Thr	Gln	Leu	Ile	Met	Pro	Gly
			580				585				
Gln	Glu	Ala	Gly	Leu	Gly	Gln	Val	Pro	Leu	Ile	Val
	590					595			600		
Gly	Ile	Leu	Leu	Val	Leu	Met	Ala	Val	Val	Leu	Ala
				605			610				
Ser	Leu	Ile	Tyr	Arg	Arg	Arg	Leu	Met	Lys	Gln	Asp
		615				620					
Phe	Ser	Val	Pro	Gln	Leu	Pro	His	Ser	Ser	Ser	His
625					630				635		
Trp	Leu	Arg	Leu	Pro	Arg	Ile	Phe	Cys	Ser	Cys	Pro
			640				645				
Ile	Gly	Glu	Asn	Ser	Pro	Leu	Leu	Ser	Gly	Gln	Gln
			650			655				660	

Val

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Val Gln Pro Val Pro Gly Ile Leu Leu Thr Leu
1 5 10
Leu Ser Gly Gln Gln Val
15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Val Gln Leu Val Pro Gly Ile Leu Leu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Val Gln Leu Val Pro Gly Ile Leu Leu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Phe Gln Leu Val Pro Gly Ile Leu Leu Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Leu Val Pro Gly Ile Leu Leu Thr Pro Pro Gln
1 5 10
Trp Ala Ala Gly Leu Ser Thr Leu Ile
15 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Leu Asp Gly Gly Asn Lys His Phe Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Val Leu Lys Arg Cys Leu Leu His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Leu Pro Ser Pro Ala Cys Gln Leu Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Leu Ala Asp Thr Asn Ser Leu Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Val Ser Val Ser Gln Leu Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Tyr Leu Glu Pro Gly Pro Val Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9
(B) TYPE: amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Asn Val Ser Leu Ala Asp Thr Asn
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGACAGGCCG AGGCAGGCCCTT TTTTTTTTTT TTTTTTTTTT
TTTTTTTTTT TTTTTTTT

40
58

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCAATCGCGA CC

12

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14
(B) TYPE: NUCLEOTIDE
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTCGCGATTG GTAA

14

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5